obtaining base sequence data of a front restriction enzyme site and base sequence data of a back restriction enzyme site, specified by a restriction enzyme used for cleaving the vector and a restriction enzyme used for obtaining the object DNA fragment, from the database;

generating a first forward retrieval key based on the obtained base sequence data of the front restriction enzyme site and a first backward retrieval key based on the obtained base sequence data of the back restriction enzyme site;

retrieving base sequence data of the recombinant DNA obtained by the search based on the first forward and first backward retrieval keys, and specifying a junction between the vector and the object DNA fragment; and

removing the vector at the specified junction.

46. The method according to Claim 45,

wherein sequence data of the first forward retrieval key and of the first backward retrieval key are generated by base sequence data of the vector entered in a vector database, data of a multiple cloning site in the vector, and data of a restriction enzyme site in the multiple cloning site,

wherein, if the restriction enzyme used to cleave the vector and the restriction enzyme used to obtain the object DNA fragment are designated, data of a forward base sequence from a cleaving point in the restriction enzyme site in the multiple cloning site of the

vector are acquired from the database, and a second forward retrieval key is generated based

on the acquired forward base sequence data of the cleaving point of the restriction enzyme site

of the vector,

performing first homology retrieval on condition that a first similarity value

between the retrieval base sequence data of the recombinant DNA and the first forward and

first backward retrieval keys is equal to or larger than a predetermined value,

obtaining a candidate for a base sequence at a junction between the vector and

the object DNA fragment according to a result of the first homology retrieval, and

performing a second homology retrieval on condition that a second similarity

value between base sequence data of a plurality of first candidates for the junction, screened by

using the first retrieval keys, and base sequence data of the second forward retrieval key, is

equal to or larger than a predetermined value.

47. The method according to Claim 45,

wherein the sequence data of the first forward retrieval key and of the first

backward retrieval key are generated by base sequence data of the vector entered in a vector

database, data of a multiple cloning site in the vector, and data of a restriction enzyme site in

the multiple cloning site,

wherein, if the restriction enzyme used to cleave the vector and the restriction

enzyme used to obtain the object DNA fragment are designated, forward base sequence data of

a forward cleaving point of the restriction enzyme site of the vector, and backward base

sequence data of a backward cleaving point of the vector are acquired from the database, and a

second forward retrieval key and a second backward retrieval key are generated based on the

base sequence data of the acquired forward and backward base sequence data of the cleaving

points, respectively,

performing a first homology retrieval on condition that a first similarity value

between the retrieval base sequence data of the recombinant DNA and the first forward and

first backward retrieval keys are equal to or larger than a predetermined value,

obtaining a candidate for a base sequence at a junction between the vector and

the object DNA fragment according to a result of the first homology retrieval, and

performing a second homology retrieval on condition that a second similarity

value between base sequence data of a plurality of first candidates for the junction, screened by

using the first retrieval keys, and base sequence data of the second forward retrieval key, is

equal to or larger than a predetermined value.

48.   The method according to Claim 47, wherein the sequence data of the first

forward and first backward retrieval keys are generated by base sequence data of the vector

entered in a vector database, data of a multiple cloning site in the vector, and data of a

restriction enzyme size in the multiple cloning site, and

wherein the second homology retrieval is performed using both the second

forward and second backward retrieval keys.

49. The method according to Claim 47,

wherein, if the restriction enzyme used to cleave the vector and the restriction enzyme used to obtain the object DNA fragment are designated, base sequence data of an area before the cleaved portion in the multiple cloning site of the vector corresponding to the designated restriction enzyme are acquired from the database, and a second forward retrieval key is generated based on the acquired base sequence data of the area before the cleaved portion, and

wherein a second homology retrieval is performed on condition that a second similarity value between base sequence data of a first candidate of a junction narrowed by a retrieval using the retrieval key and base sequence data of the second forward retrieval key is equal to or larger than a predetermined value.

50. The method according to Claim 45,

wherein, if the restriction enzyme used to cleave the vector and a restriction enzyme used to obtain the object DNA fragment are designated, backward base sequence data from a cleaving point in a multiple cloning site of the vector corresponding to the designated restriction enzyme are acquired from the database, and a second backward retrieval key is generated based on the acquired backward base sequence data of the cleaving point, and

performing a first homology retrieval on condition that a first similarity value

between the retrieval base sequence data of the recombinant DNA and the first forward and

first backward retrieval keys are equal to or larger than a predetermined value;

obtaining a candidate for a base sequence at a junction between the vector and

the object DNA fragment according to a result of the first homology retrieval; and

performing a second homology retrieval on condition that a second similarity

value between base sequence data of a first candidate for the junction, screened by using the

first retrieval keys, and base sequence data of the second backward retrieval key is equal to or

larger than a predetermined value.

51. The method according to Claim 50,

wherein said vector is removed from the recombinant DNA sequence data, when

the area specified by the second homology retrieval is one.

52. The method according to Claim 47, further comprising:

obtaining, as a forward vector unit candidate for the vector base sequence, a

forward base sequence specified as a result of the second homology retrieval and a base

sequence before said forward base sequence; and

obtaining, as a backward vector unit candidate for the vector base sequence, a

backward base sequence specified as a result of the second homology retrieval and a base

sequence after said backward base sequence.

53.   The method according to Claim 51,

wherein said forward vector unit candidate and said backward vector unit

candidate are removed from the recombinant DNA sequence data, when there is only one

candidate respectively for the specified forward and backward vector units, and the specified

forward and backward vector units do not overlap each other.

54.   A device for removing a vector from a recombinant DNA base sequence,

obtained as a result of performing a cloning process by integrating an object DNA fragment

into a vector, comprising:

a database storing data of a restriction enzyme, and data of base sequences of a

restriction enzyme site of a plurality of vectors;

an obtaining unit obtaining base sequence data of a front restriction enzyme site

and base sequence data of a back restriction enzyme site, specified by the restriction enzyme

used for cleaving the vector and the restriction enzyme used for obtaining the object DNA

fragment, from the database;

a generation unit generating a first forward retrieval key based on the obtained

base sequence data of the front restriction enzyme site of a vector, and a first backward

retrieval key based on the base sequence data of the back restriction enzyme site; and

a retrieving unit retrieving base sequence data of the recombinant DNA obtained based on the first forward and first backward retrieval keys, and specifying a junction between the vector and the object DNA fragment based on the retrieval result.

55. The device according to Claim 54, further comprising:

display means,

wherein said vector is included in a vector list displayed on said display means, and

wherein at least one of said specified restriction enzymes is included in a restriction enzyme list displayed on said display means.

56. The device according to Claim 54, further comprising:

program storage means for storing at least one of:

a program for generating the retrieval keys by controlling said generation unit;

a program for specifying the vector base sequence by controlling said retrieving unit; and

a program for removing the vector base sequence.

57. The device according to Claim 54,

wherein said retrieving unit specifies using the first retrieval key as a junction

between the vector base sequence data and the object DNA fragment sequence data.

58.   The device according to Claim 57,

wherein said retrieving unit specifies, as the junction, a portion in the DNA base

sequence data in which a number of bases matching a base sequence of the first retrieval key is

equal to or larger than a predetermined value.

59.   The device according to Claim 54,

wherein said retrieving unit specifies using, as the first retrieval key, a first

junction and a second junction between the vector base sequence and the object DNA

fragment.

60.   The device according to Claim 54,

wherein said retrieval key is first forward and first backward retrieval keys

including sequence data including an end portion of the object DNA fragment and sequence

data including an end portion of the vector base sequence, and specifies a candidate for a

junction between the vector base sequence and the object DNA fragment.

61.   The device according to Claim 60,

wherein a second retrieval key, including sequence data longer than that of said

first forward and first backward retrieval keys, is generated, and the junction is specified using

the second retrieval key.

62.   The device according to Claim 61,

        wherein said object DNA fragment is specified by removing the junction and

sequence data distal to the junction and the object DNA fragment from the DNA base

sequence.

63.   A computer-readable storage medium on which is recorded a program enabling

a computer to execute an operation process of a base sequence of a recombinant DNA obtained

by integrating an object DNA into a vector, said process comprising the steps of:

        storing data of a restriction enzyme and data of a base sequence of a restriction

enzyme site of a plurality of vectors in a database;

        obtaining base sequence data, of a front restriction enzyme site and base

sequence data of a back restriction enzyme site, specified by the restriction enzyme used for

cleaving the vector and the restriction enzyme used for obtaining the object DNA fragment,

from the database;

        generating a forward retrieval key based on the obtained base sequence data of

the front restriction enzyme site, and a backward retrieval key based on the obtained base

sequence data of the back restriction enzyme site;